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LIST OF CLAIMS, SHOWING THE STATUS OF EACH CLAIM

Underlining denotes added text while strikethrough denotes deleted text.

IN THE CLAIMS:

1. (Currently Amended) A cutinase variant comprising substitution of the residue positions corresponding to sites 192 ~~and/or 194~~, of the *Pseudomonas mendocina* cutinase set forth in SEQ ID NO: 2, and wherein said variant has increased polyesterase activity and enhanced thermostability, as compared to wild-type *Pseudomonas mendocina* cutinase.

Claims 2-18. (Cancelled)

19. (Currently Amended) The cutinase of claim 1, wherein said variant comprises the following substitutions: Met at position 192, and further comprising the substitutions of Val at position 194, and Ser at position 219, ~~wherein said variant has enhanced polyesterase activity, in comparison with wild-type *P. mendocina* cutinase.~~

Claims 20-27. (Cancelled)

28. (Currently Amended) A cutinase variant comprising substitution of the residue positions corresponding to sites 192 ~~and/or 194~~, of the *Pseudomonas mendocina* cutinase set forth in SEQ ID NO:-2, ~~and~~ wherein said variant is more thermostable than wild-type *P. mendocina* cutinase, and wherein said cutinase variant has hydrolytic activity on polyester.

29. (Cancelled)

30. (Currently Amended) The cutinase variant of claim 28, wherein said variant further comprises a substitution of the amino acid residue at position 219 of *Pseudomonas mendocina* cutinase SEQ ID NO:-2.

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31. (Currently Amended) The cutinase variant of claim 1, wherein said variant further comprises a substitution of the amino acid residue at position 219 of *Pseudomonas mendocina* cutinase SEQ ID NO: 2.

32. (Cancelled)

33. (Currently Amended) The cutinase variant of claim 30, wherein the residue at position 194 is substituted with one of Ala, His, Lys, Leu, Asn, Pro or Gly, and said residue at position 219 is substituted with Gly.

34. (Currently Amended) The cutinase variant of claim 1, wherein said variant comprises a substitution of the residue at position 194 with one of Ala or His, and a substitution at 219 with Gly, ~~wherein said variant has enhanced polyesterase activity in comparison with wild type *P. mendocina* cutinase.~~

35. (Currently Amended) The cutinase variant of claim 1, wherein said variant comprises a substitution at position 194 with Ile, ~~wherein said variant has enhanced polyesterase activity in comparison with wild type *P. mendocina* cutinase.~~

36. (Currently Amended) The cutinase variant of claim 1, wherein said variant comprises a substitution at position 194 with one of Lys or Leu and substitution at position 219 with Gly ~~wherein said variant has enhanced polyesterase activity in comparison with wild type *P. mendocina* cutinase.~~

37. (Currently Amended) The cutinase variant of claim 1, wherein said variant comprises the substitution of Asn at position 194, ~~wherein said variant has enhanced polyesterase activity in comparison with wild type *P. mendocina* cutinase.~~

38. (Currently Amended) The cutinase variant of claim 1, wherein said variant comprises the substitution of the residue at position 194 with one of Asn, Pro, or Ser, and substitution of the residue at position 219 with Gly, ~~wherein said variant has enhanced polyesterase activity in comparison with wild type *P. mendocina* cutinase.~~

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39. (New) A cutinase variant comprising substitution of the residue positions corresponding to site 194, of the *Pseudomonas mendocina* cutinase set forth in SEQ ID NO:2, and wherein said variant has increased polyesterase activity and enhanced thermostability, as compared to wild-type *Pseudomonas mendocina* cutinase.

40. (New) The cutinase variant of claim 39, wherein said variant further comprises the substitutions of Met at position 192, Val at position 194, and Ser at position 219.

41. (New) The cutinase variant of claim 39, wherein said variant comprises a substitution of the residue at position 194 with Ile, Leu, Asn, or Pro.

42. (New) A cutinase variant comprising substitution of the residue position corresponding to site 194 of the *Pseudomonas mendocina* cutinase set forth in SEQ ID NO:2, and wherein said variant is more thermostable than wild-type *P. mendocina* cutinase, and wherein said cutinase variant has hydrolytic activity on polyester.

43. (New) The cutinase variant of claim 42, wherein said variant further comprises a substitution of the amino acid residue at position 219 of *Pseudomonas mendocina* cutinase SEQ ID NO:2.

44. (New) The cutinase variant of claim 39, wherein said cutinase variant further comprises a substitution of the amino acid residue at position 219 of *Pseudomonas mendocina* cutinase SEQ ID NO:2.

45. (New) The cutinase variant of claim 43, wherein said residue at position 194 is substituted with Ala, His, Lys, Leu, Asn, Pro or Gly, and said residue at position 219 is substituted with Gly.

46. (New) The cutinase variant of claim 39, wherein said variant comprises a substitution of the residue at position 194 with Ala or His, and substitution at position 219 with Gly.

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47. (New) The cutinase variant of claim 39, wherein said variant comprises a substitution at position 194 with Ile.
48. (New) The cutinase variant of claim 39, wherein said variant comprises a substitution at position 194 with Lys or Leu, and substitution at position 219 with Gly.
49. (New) The cutinase variant of claim 39, wherein said variant comprises the substitution of Asn at position 194.
50. (New) The cutinase variant of claim 39, wherein said variant comprises the substitution of the residue at position 194 with Asn, Pro, or Ser, and substitution of the residue at position 219 with Gly.